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Computational modelling of person-environment transactions

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Genetic influences

- From twin data:
 - Pervasive across breadth and flavour of traits
 - About 50% of phenotypic variance heritable
- From family and adoption data:
 - Estimates somewhat weaker
- From molecular genetic data (GCTA)
 - Estimates yet weaker

Why?

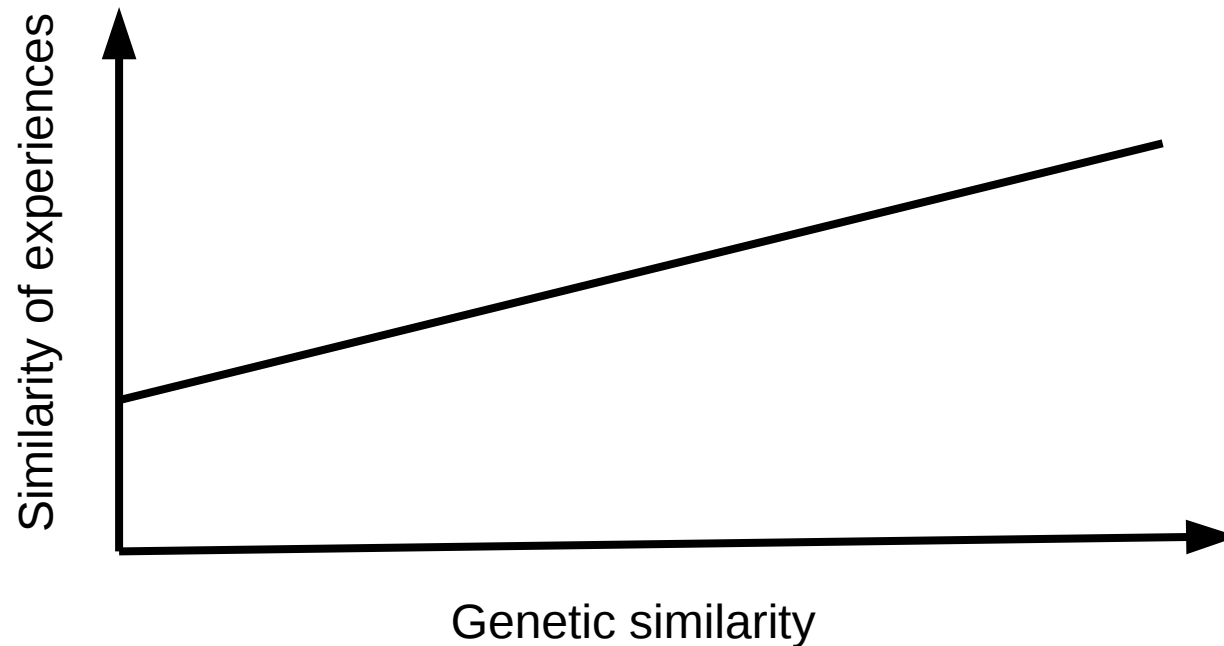
- Traits highly polygenic
 - Zillion polymorphisms, each with a minor effect
- Rare variants
- Missing heritability

- Additive heritability estimates inflated
 - Person-environment transactions (PET)
 - Pervasive personality influences on life choices
 - Positive feedback loops make genetically similar people phenotypically yet more similar

- Genetic variance 'non-additive'
 - Phenotypic similarity increases exponentially with genetic similarity
 - Small genetic differences can lead to relatively larger phenotypic differences
 - Family/adoption studies and GCTA address only additive variance

- I will address both simultaneously
 - PET and non-additive variance

- Does PET contribute to additive influence?
 - Genetic similarity linearly related to environmental similarity
 - No idea
 - Why think otherwise if we consider only one trait at a time?

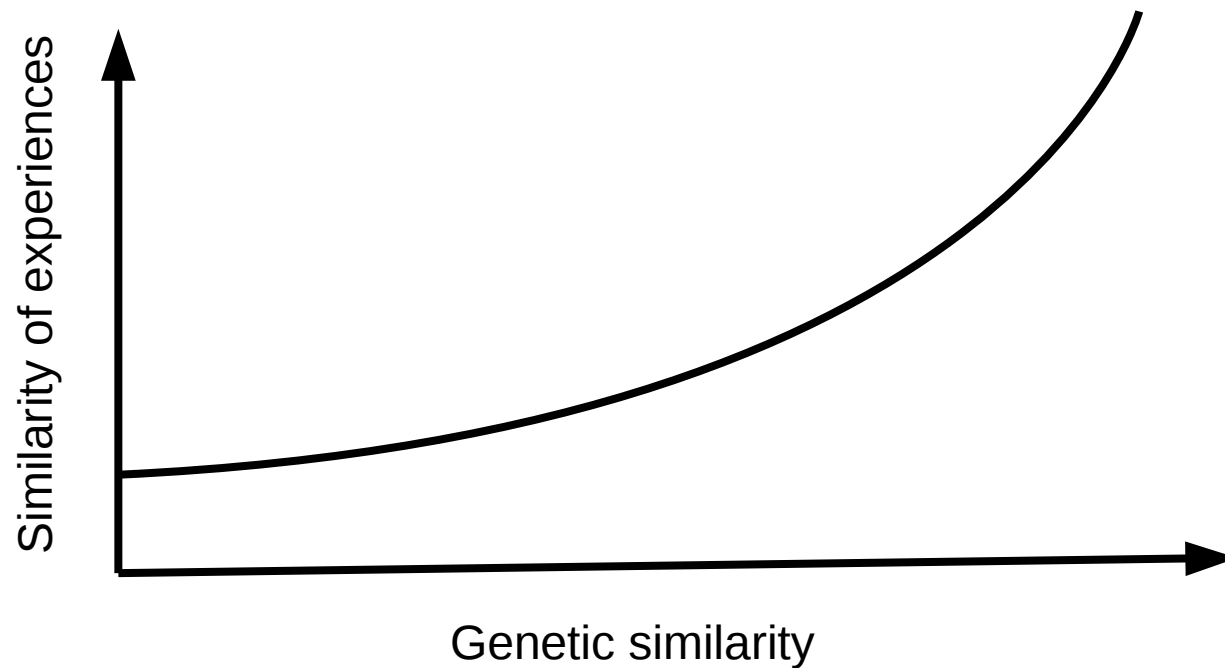


Multi-trait perspective

- Perhaps people do not transact with environments based on all characteristics
 - Salient (central, most expressed) traits for niche-picking



- Genetic differences increase the likelihood of different characteristics being salient
 - Even small genetic difference may lead to very different environments
 - Results in increasing phenotypic differences



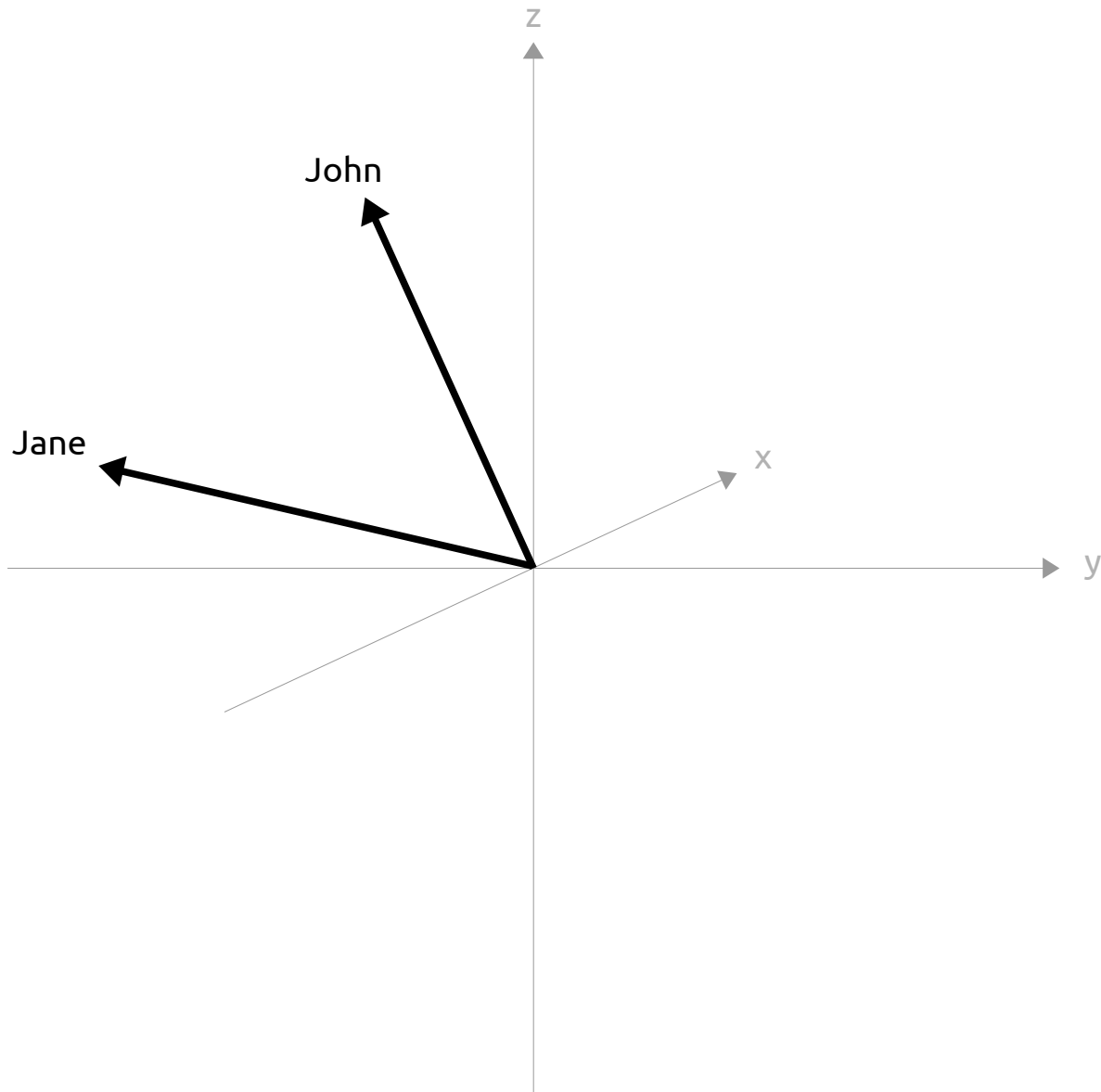
Hypothesis

- Non-additive variance is (also) PET in disguise
 - Especially when PET are based on limited traits

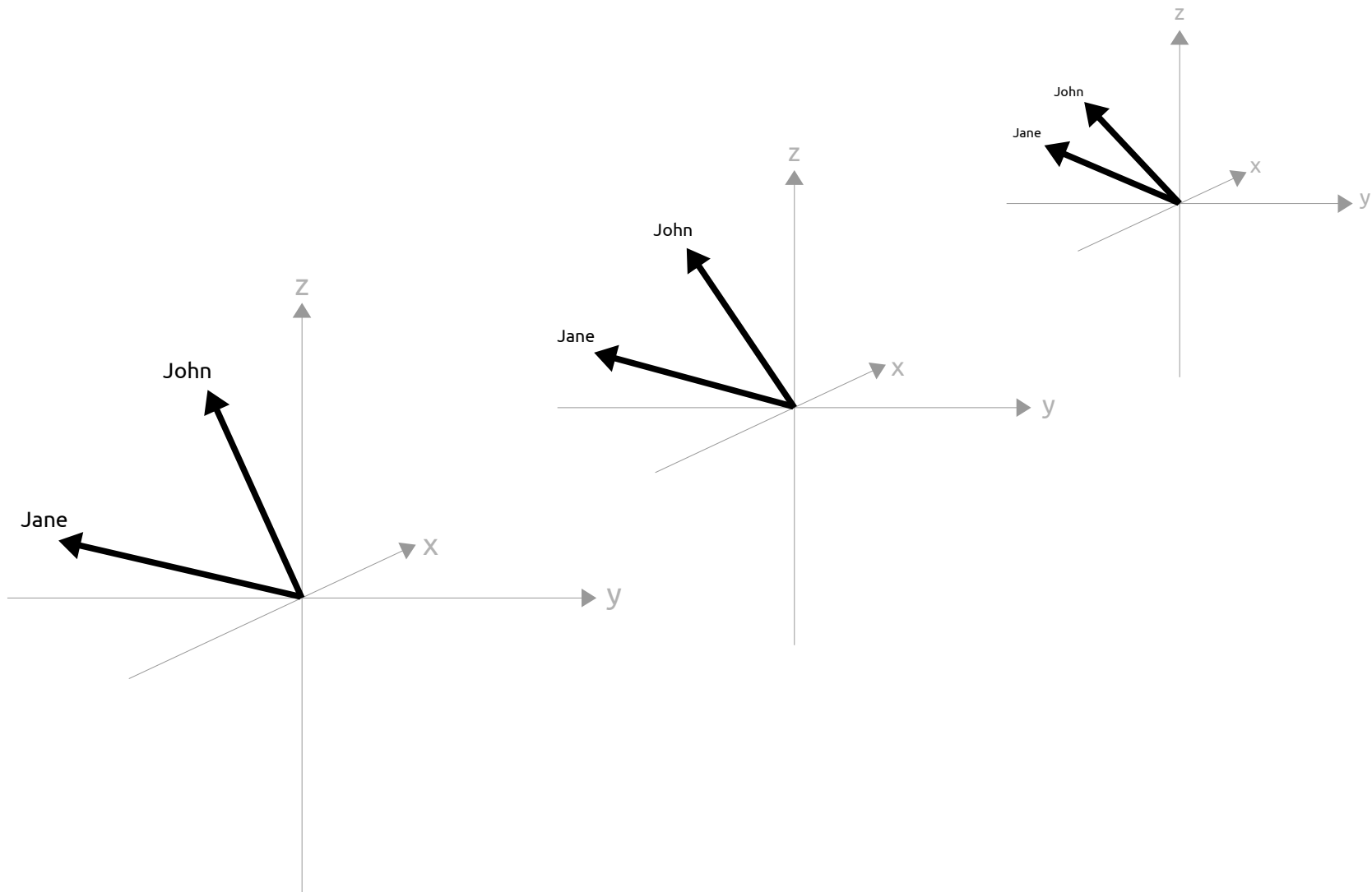
Different scenarios of a computational model

- PET absent vs PET present
- PET based on varying proportions of traits
- Expectation:
 - Smaller proportions yield more 'non-additive' variance

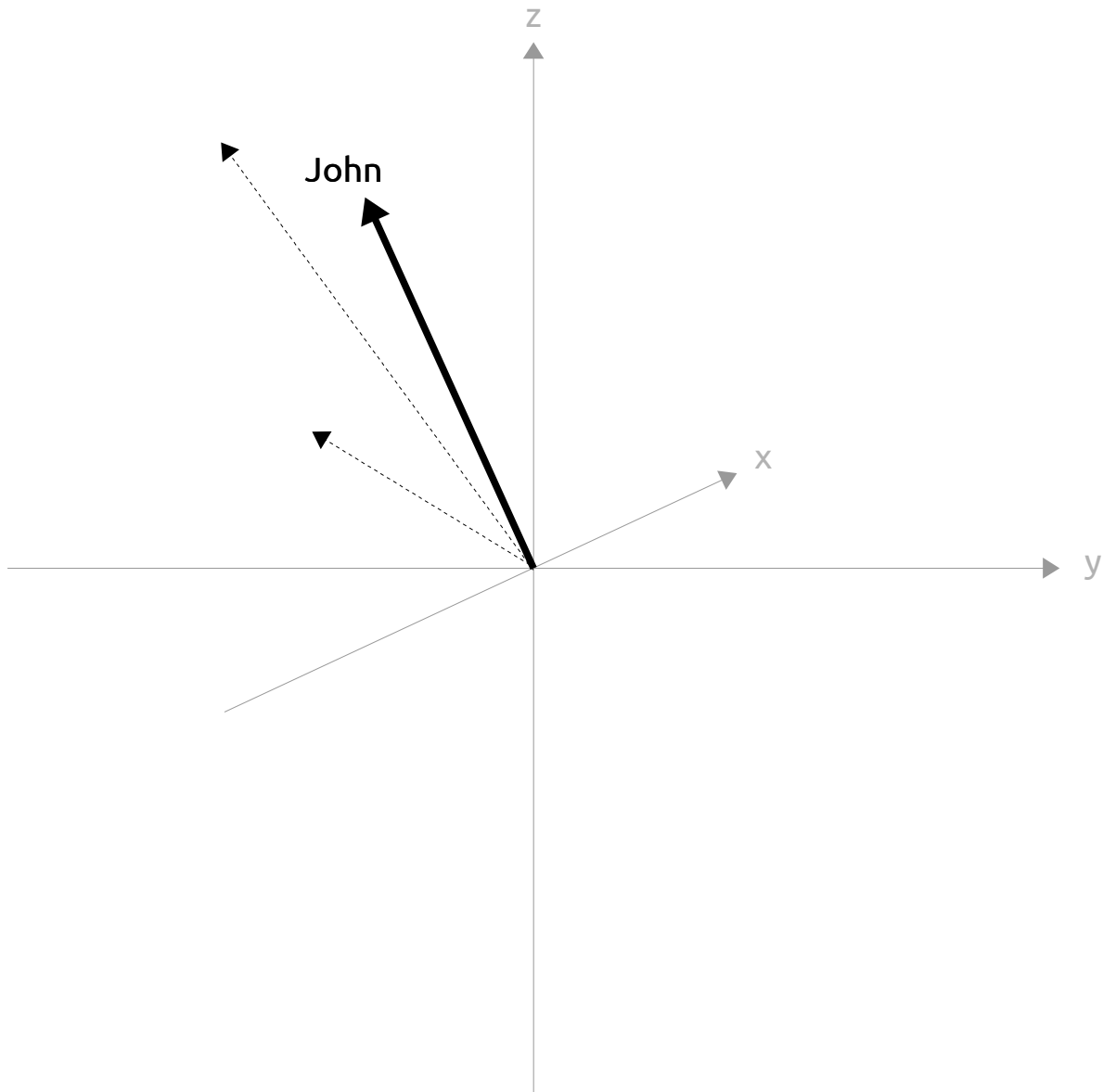
Computational model framework



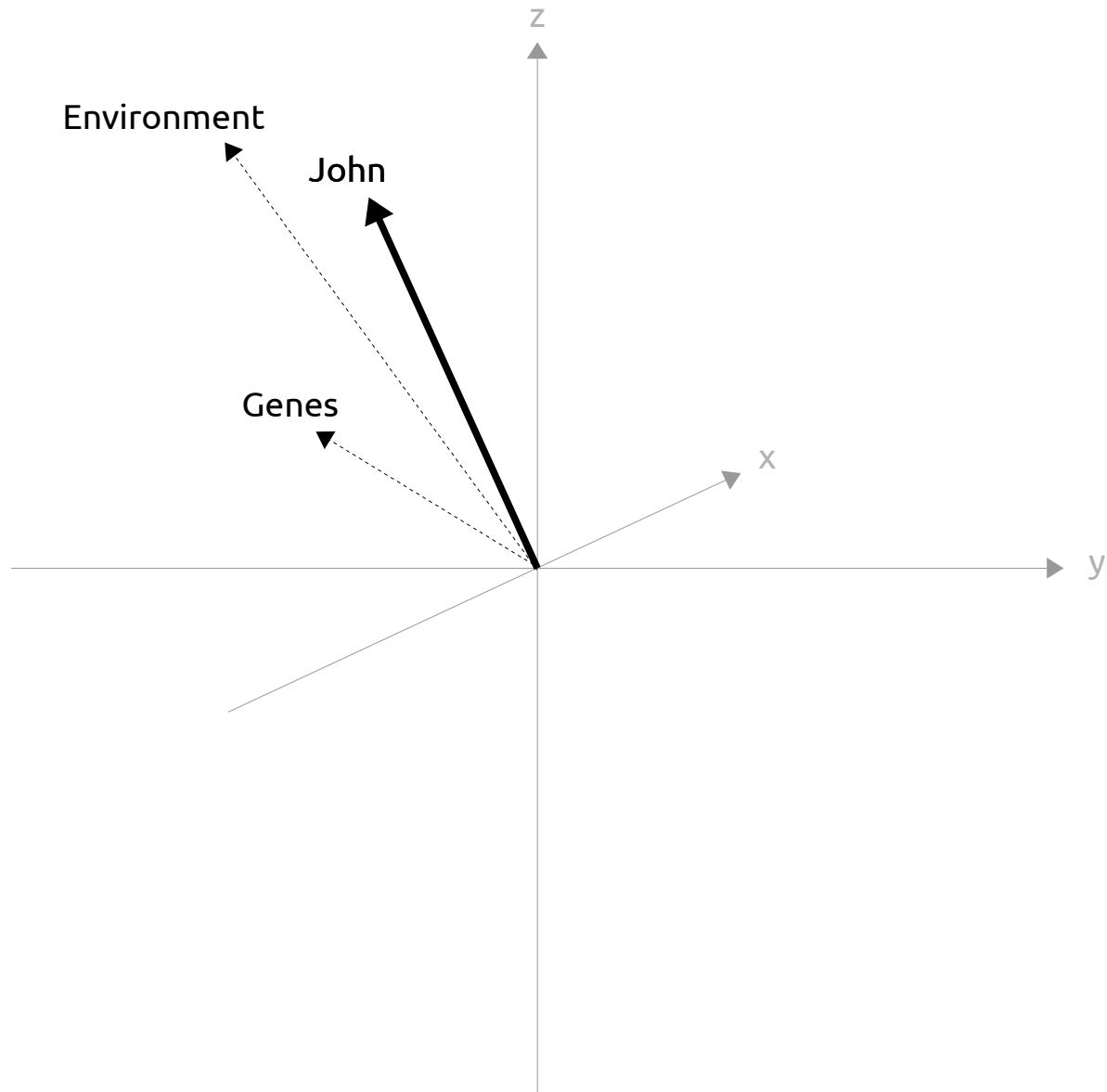
The feature space may have a zillion dimensions



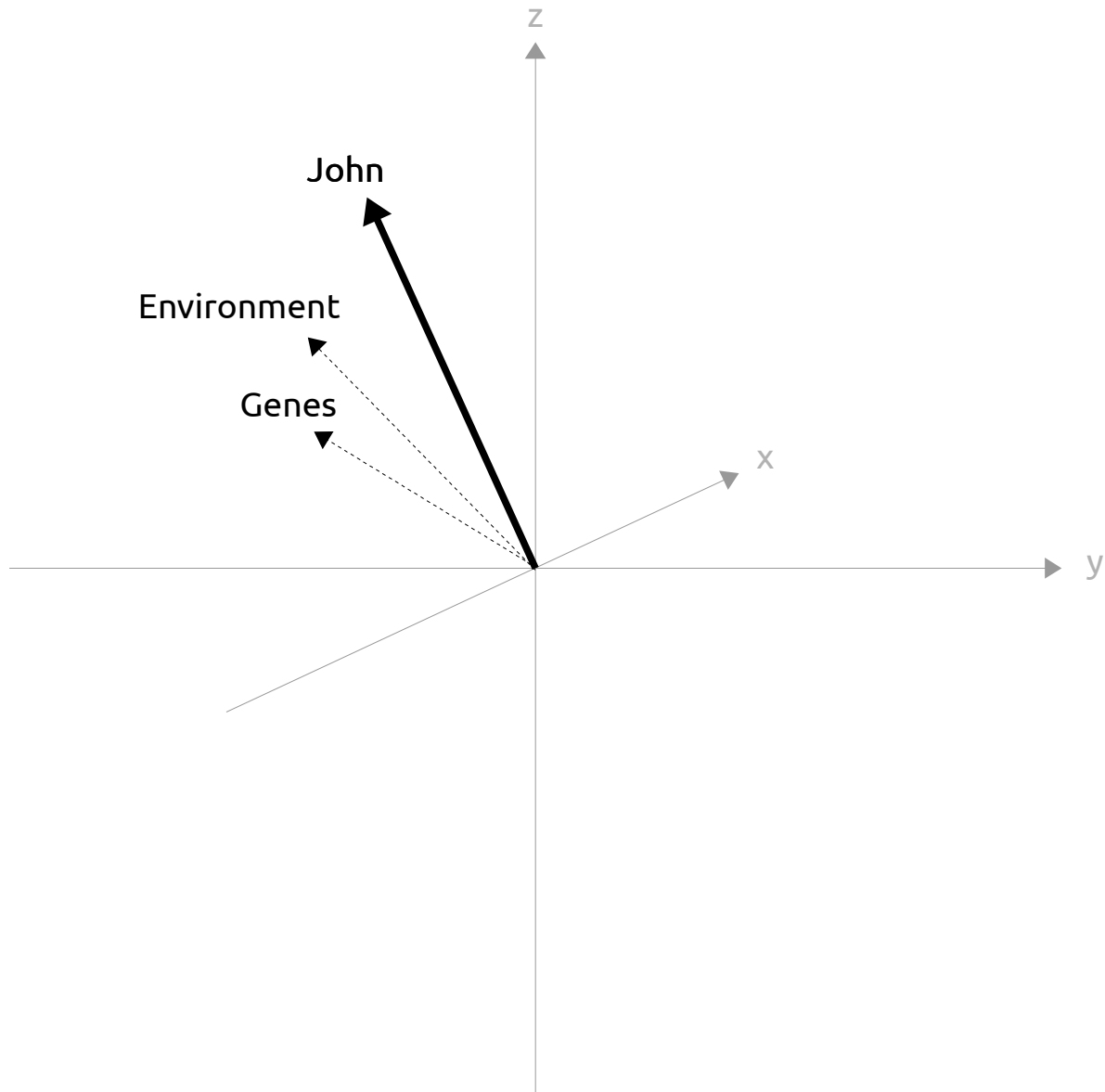
Development through discrete cycles



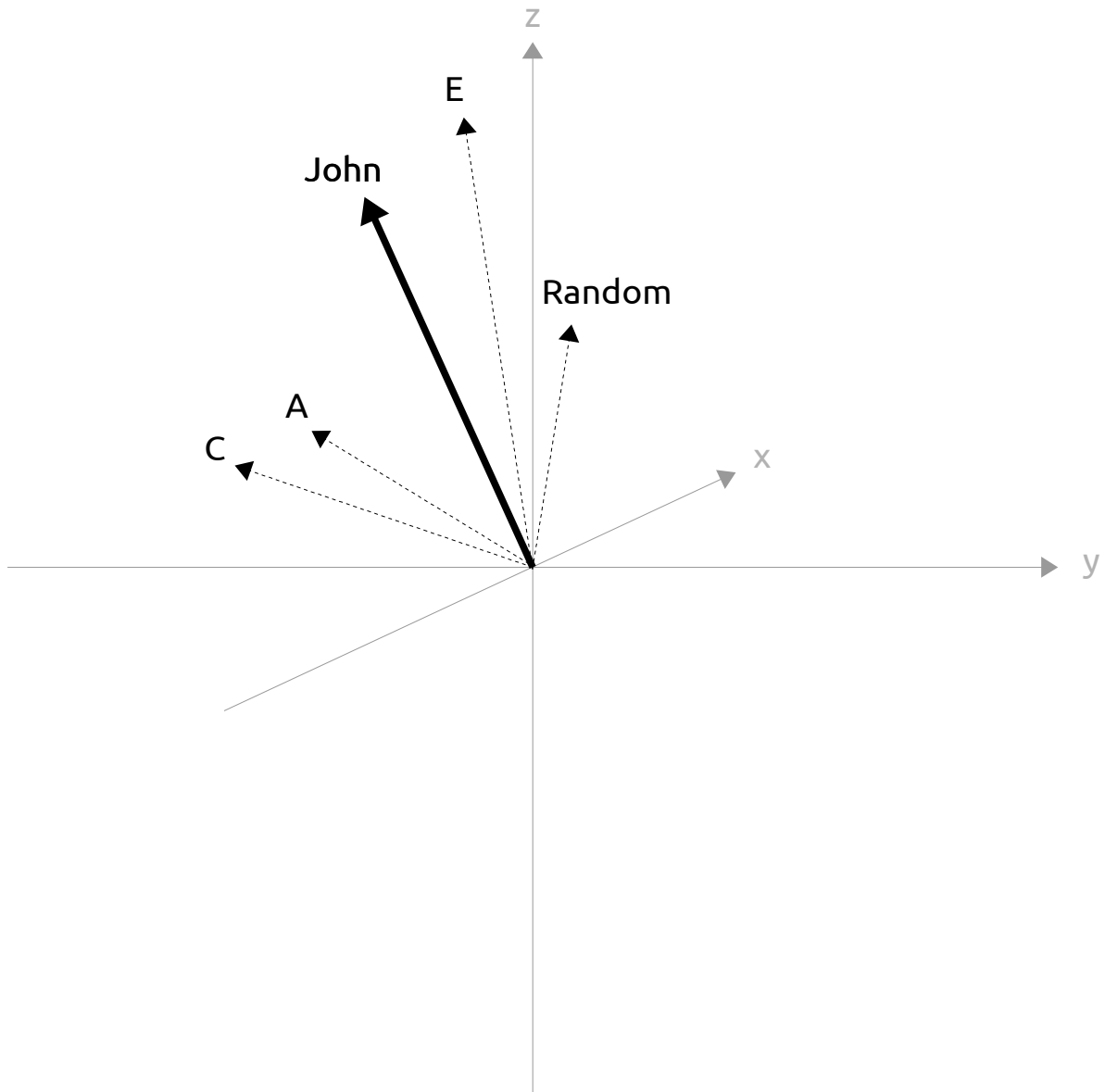
The feature space is also a force field

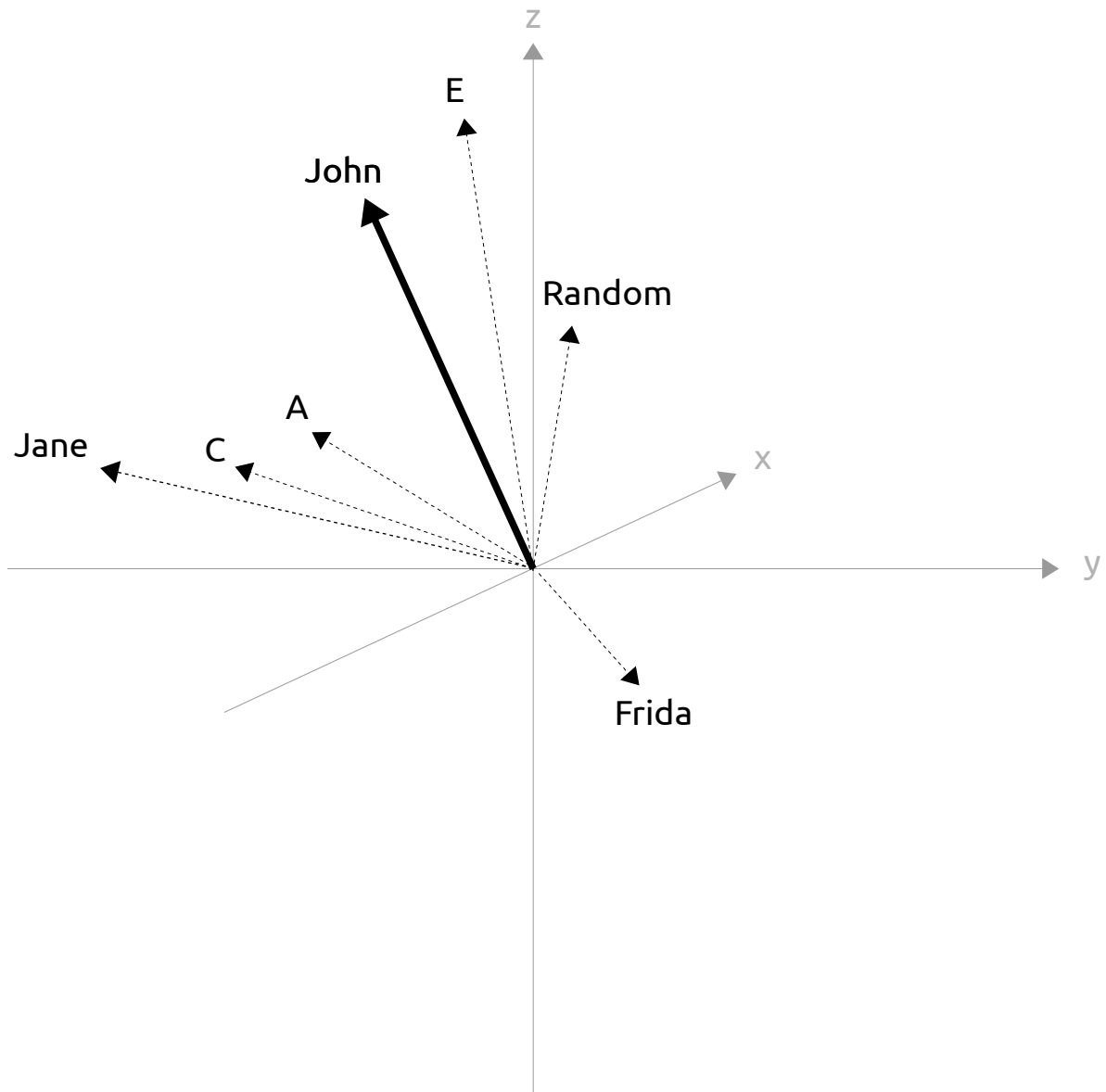


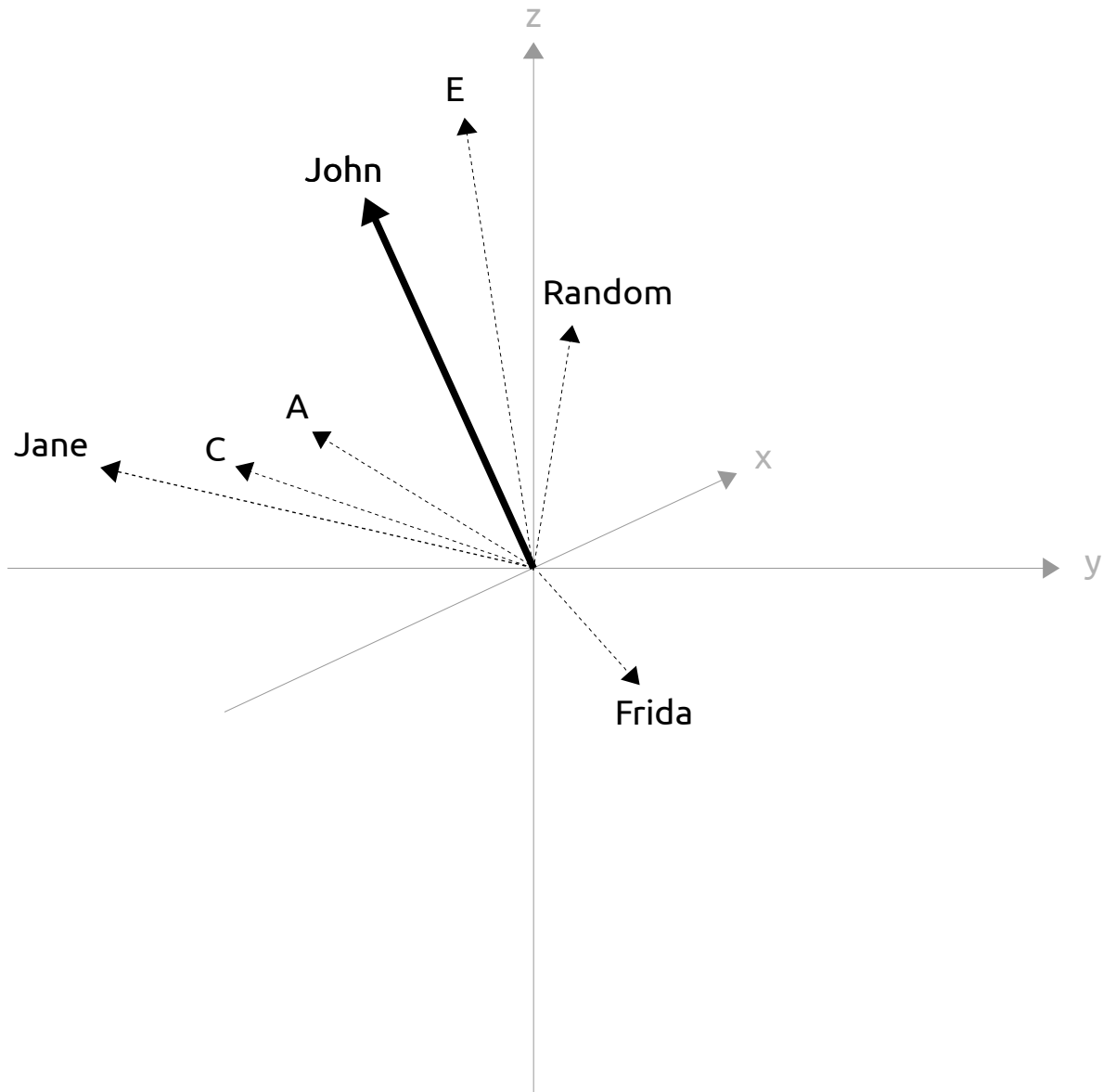
The feature space is also a force field



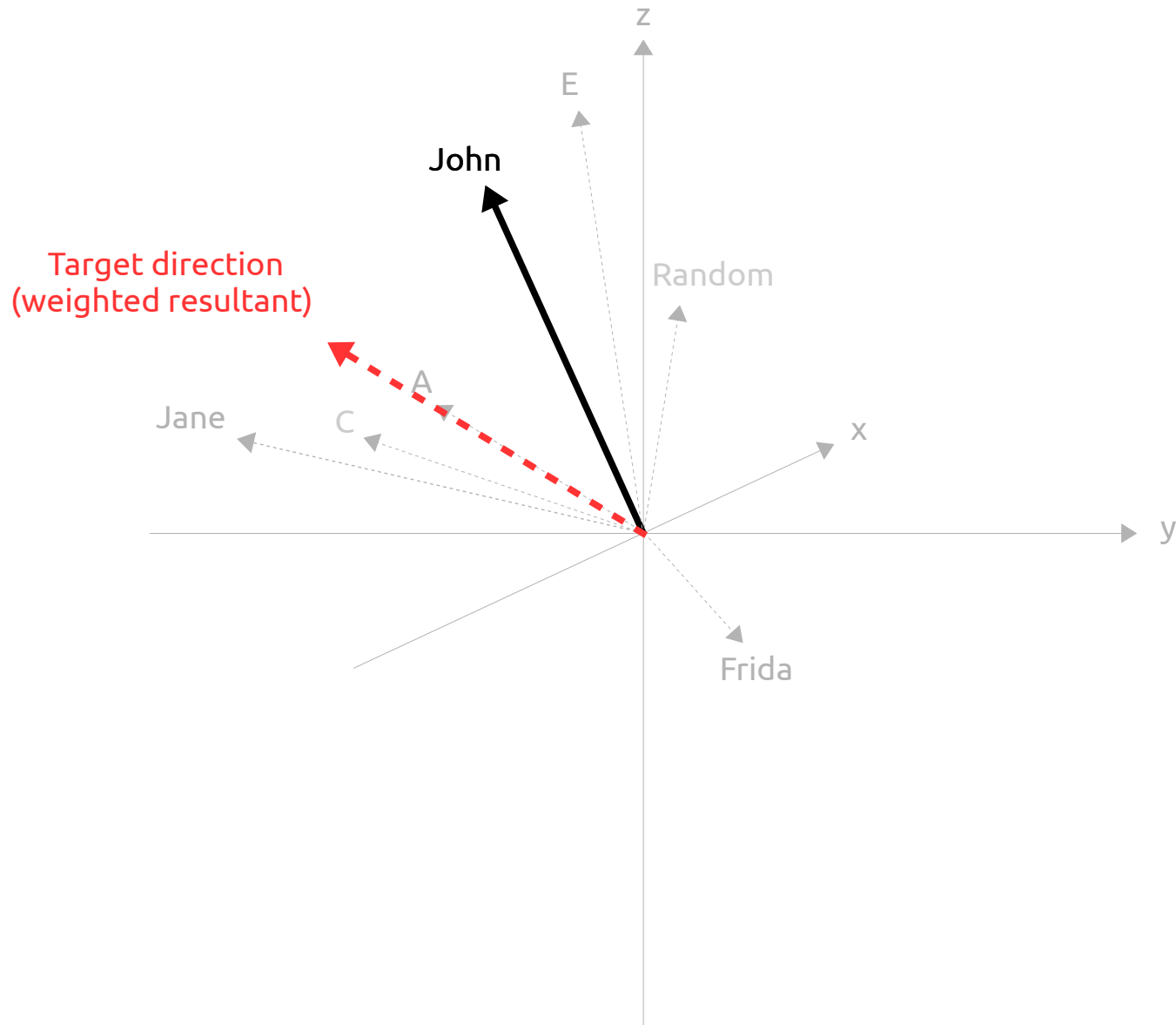
The feature space is also a force field







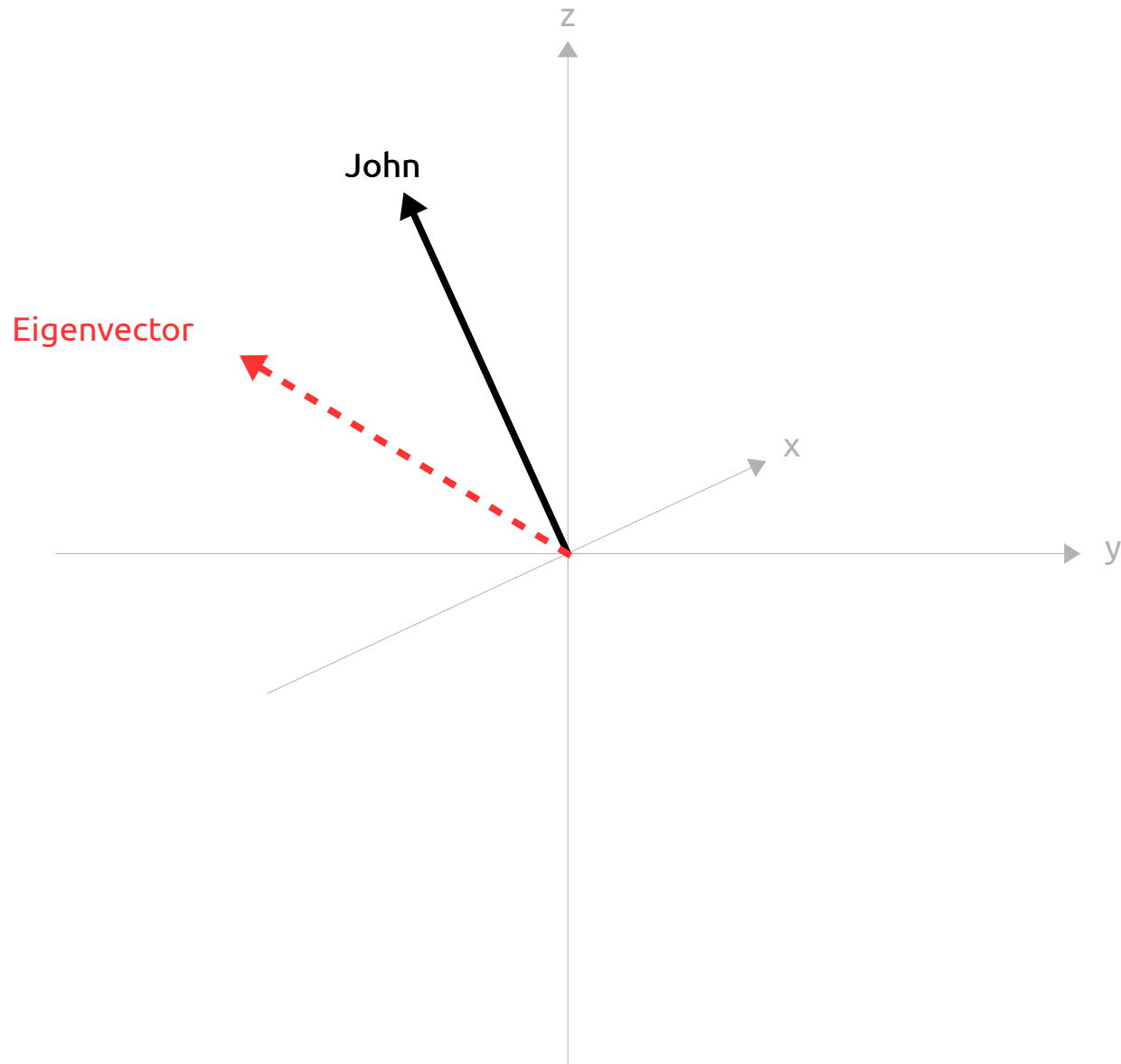
Different forces can have different weights



At every cycle, John is attracted to the target direction

Updating an individuals location (at any one cycle)

new scores = weight matrix * previous scores



Target direction is the eigenvector of the weight matrix

Step 1 Translate target direction to weight matrix

$$\begin{pmatrix} -.50 \\ -.50 \\ .00 \end{pmatrix} \quad \Rightarrow \quad \text{Oblique projection} \quad \Rightarrow \quad \begin{pmatrix} -.26 & -.29 & .00 \\ -.22 & -.24 & .00 \\ .00 & .00 & -.50 \end{pmatrix}$$

Step 2 Project person vector towards target direction

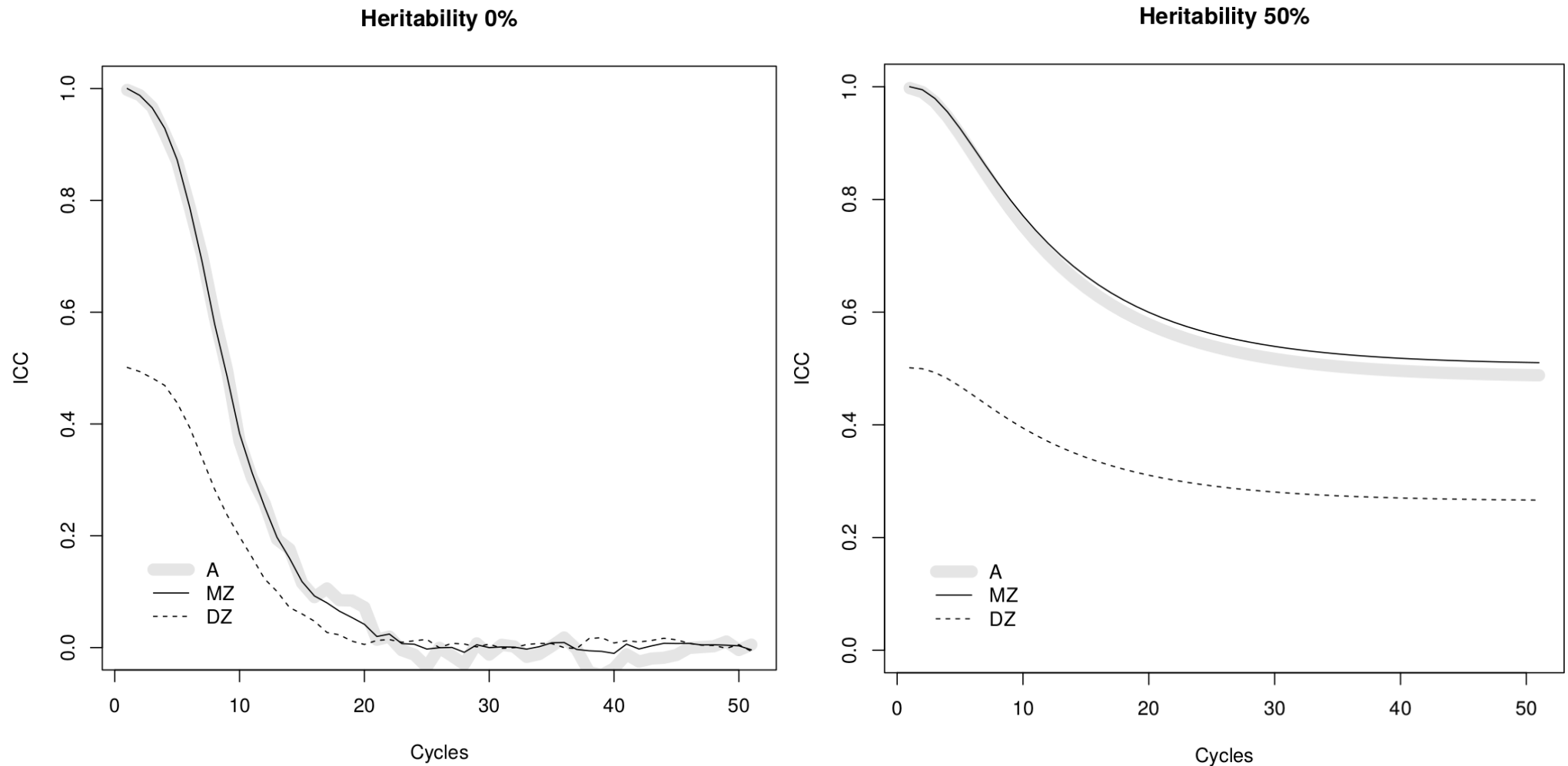
$$\begin{pmatrix} -.26 & -.29 & .00 \\ -.22 & -.24 & .00 \\ .00 & .00 & -.50 \end{pmatrix} * \begin{pmatrix} -.50 \\ -.50 \\ 1.00 \end{pmatrix}$$

PET ~ social interactions

- Individuals tend to become like 'friends'
- Similar individuals more likely to interact
 - Direct selection, picking similar niches (“social homogamy”)
- Individuals become parts of their own environment
- Initially similar become more similar
 - By reinforcing their own and 'friends' traits

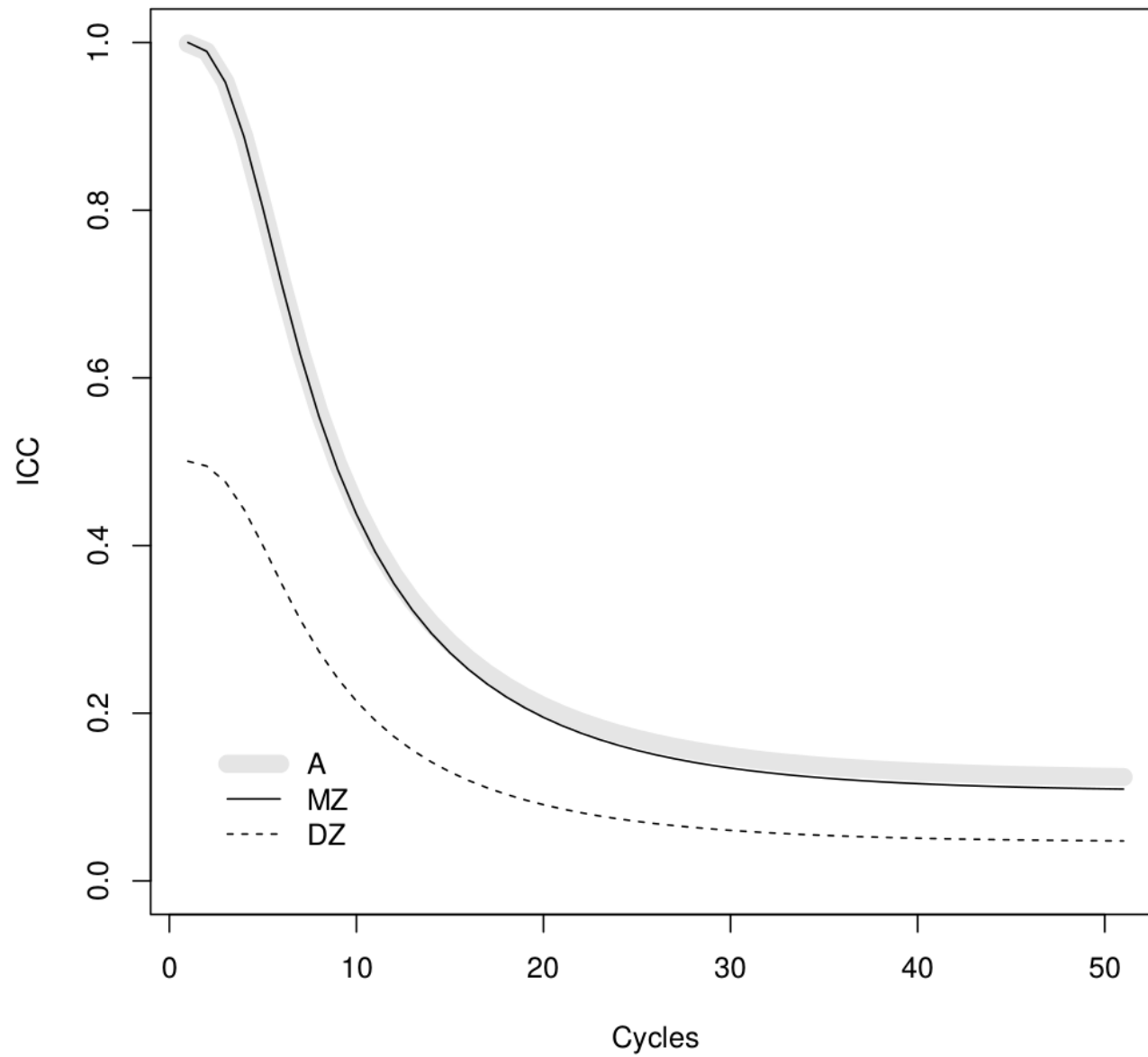
- 50 traits develop through 50 cycles
- Twin structure: 500 'twin pairs'
 - 250 genetically identical, 250 half-identical
- Initial trait levels 100% genetic
 - Oversimplification
 - But heritability is very high in childhood
 - Kept constant in all scenarios

Sanity check: no social interactions

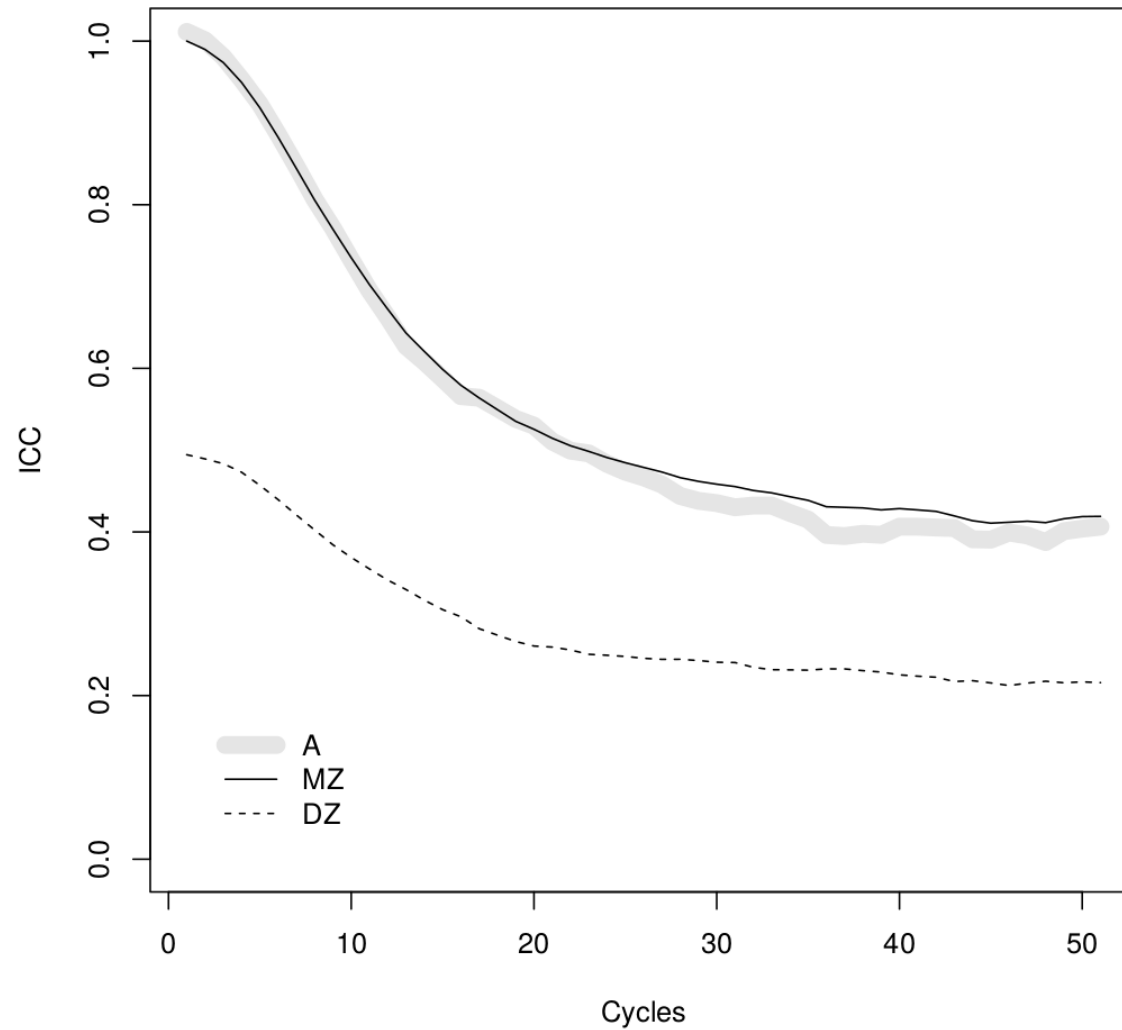


Average estimates across the 50 traits

Heritability 10%, stable unique factors 90%

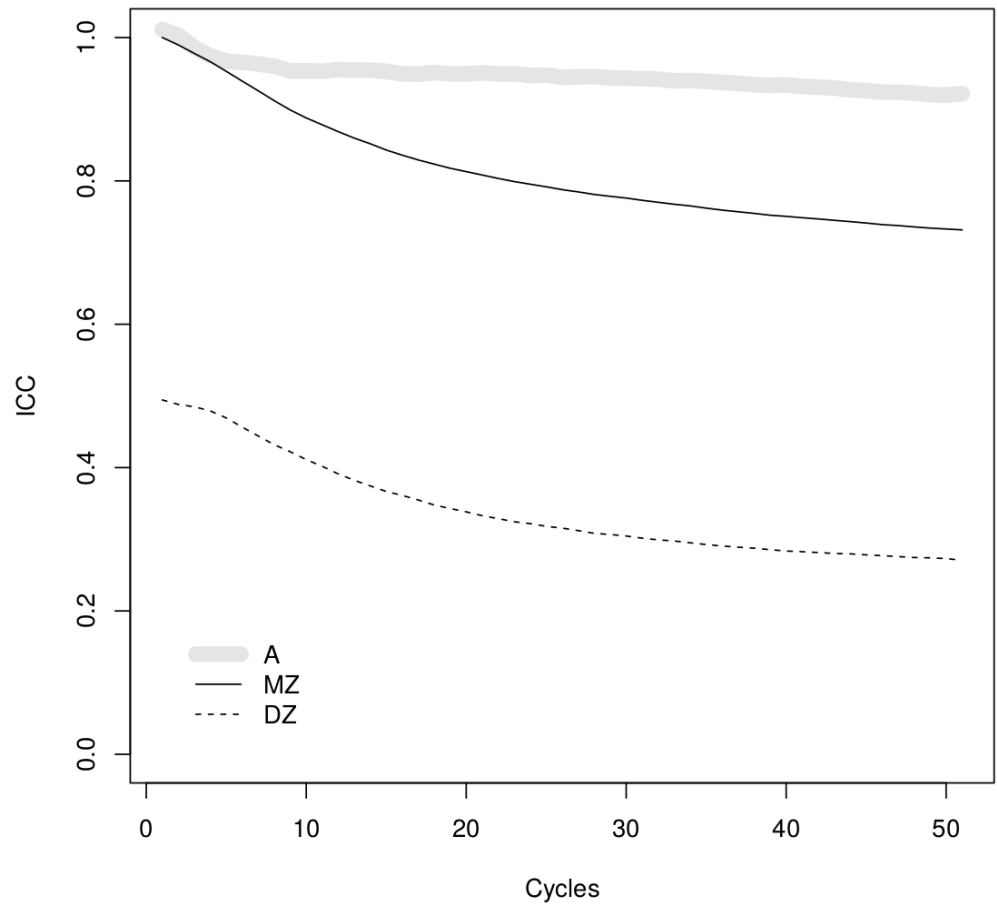


Heritability 10%, stable unique factors 10%, random influences 80%

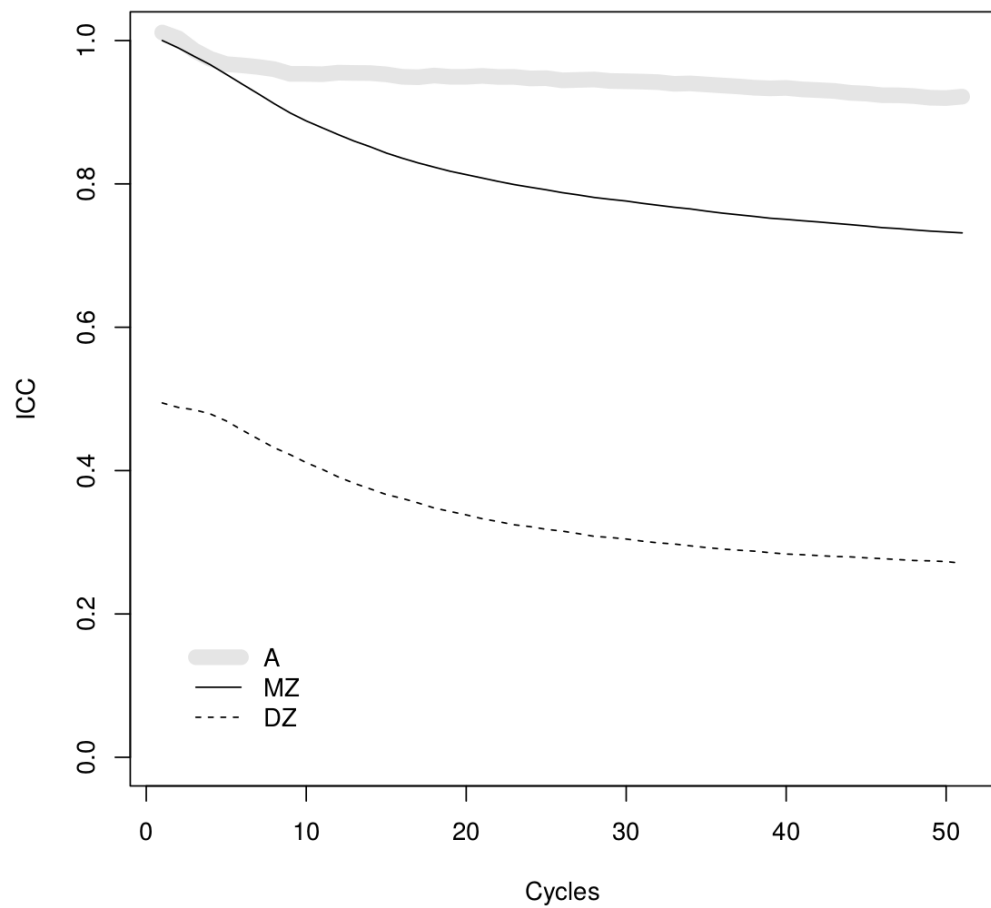


- Transient random influences not enough to weed out initial strong genetic influences
 - Individuals wiggle into largely genetic niches

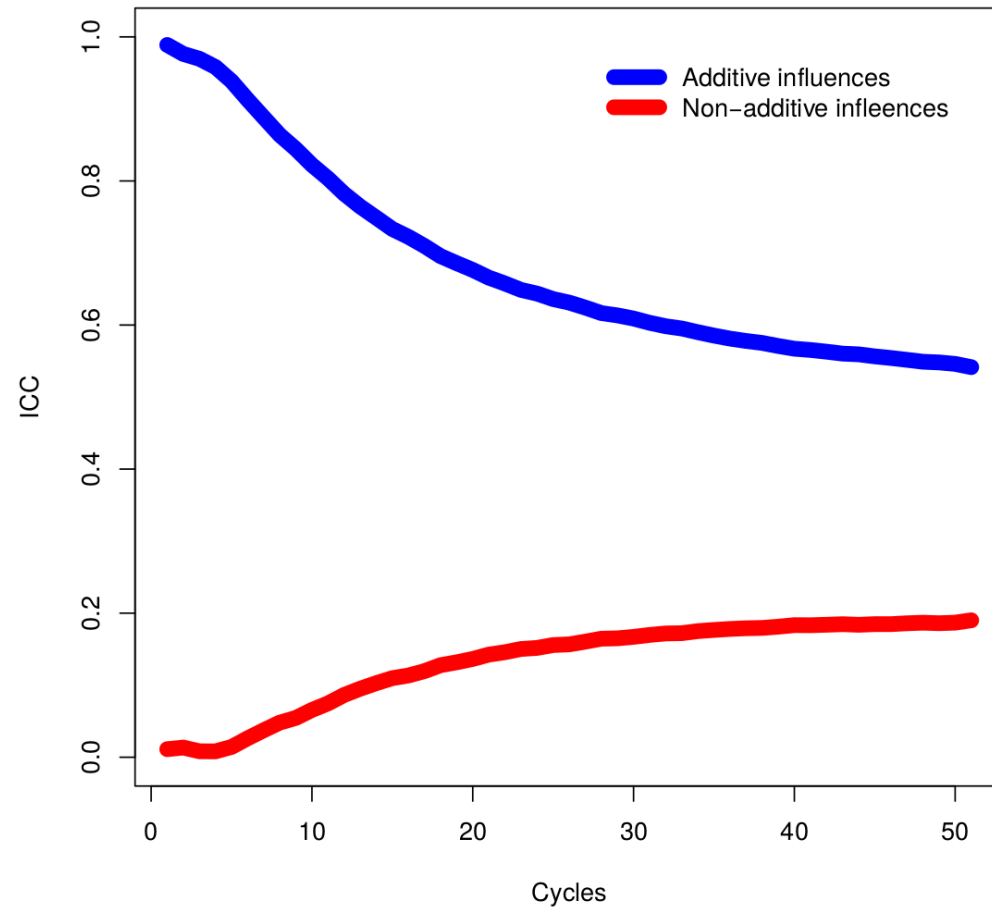
Heritability 10%, stable unique factors 10%, PET 80%



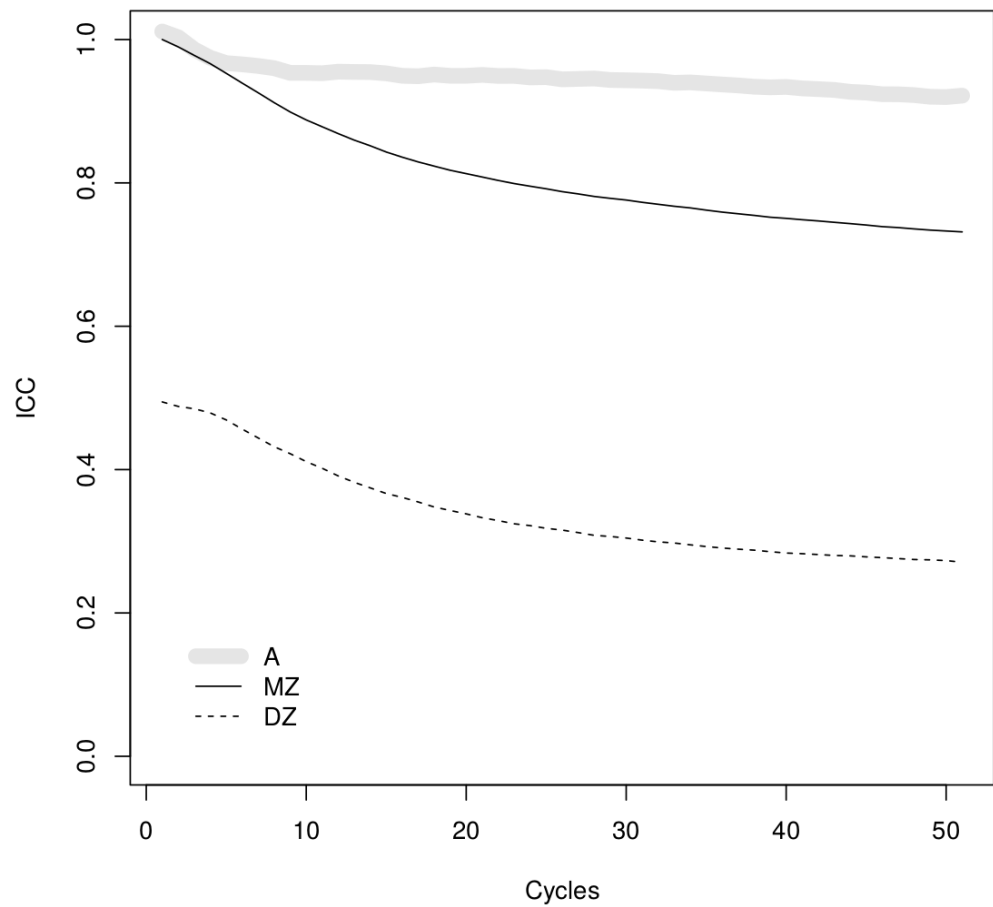
Heritability 10%, stable unique factors 10%, PET 80%



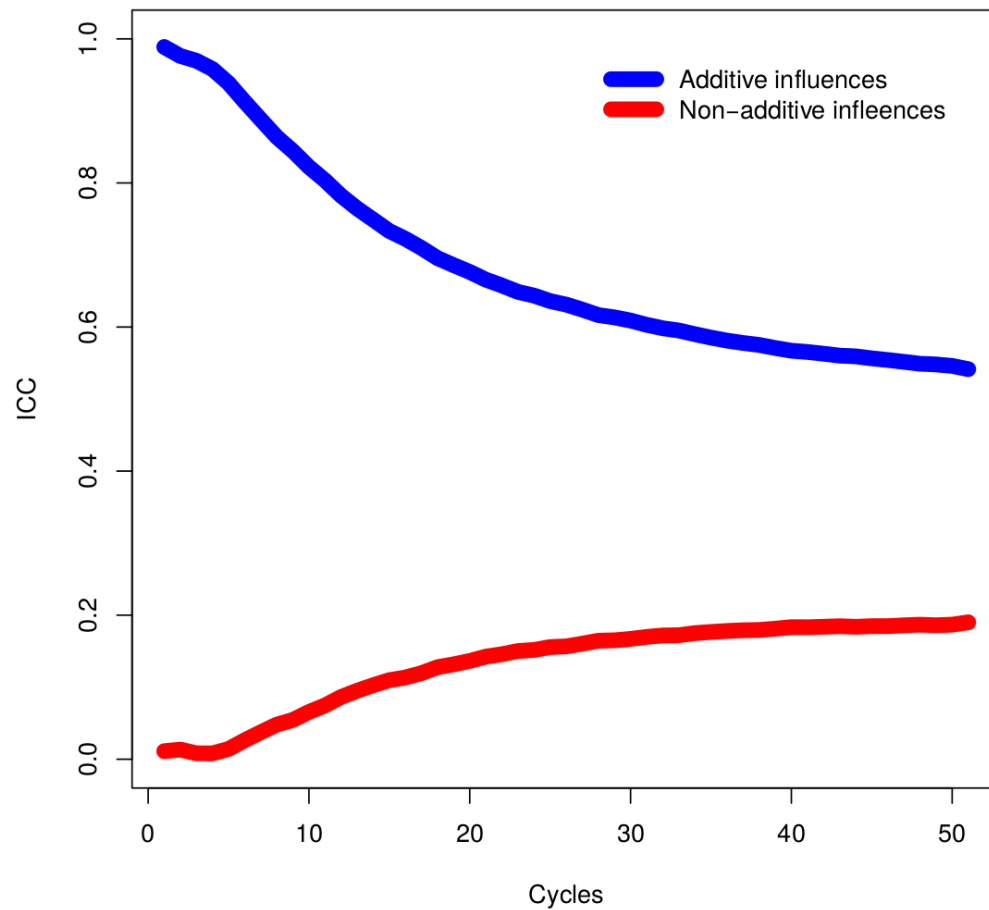
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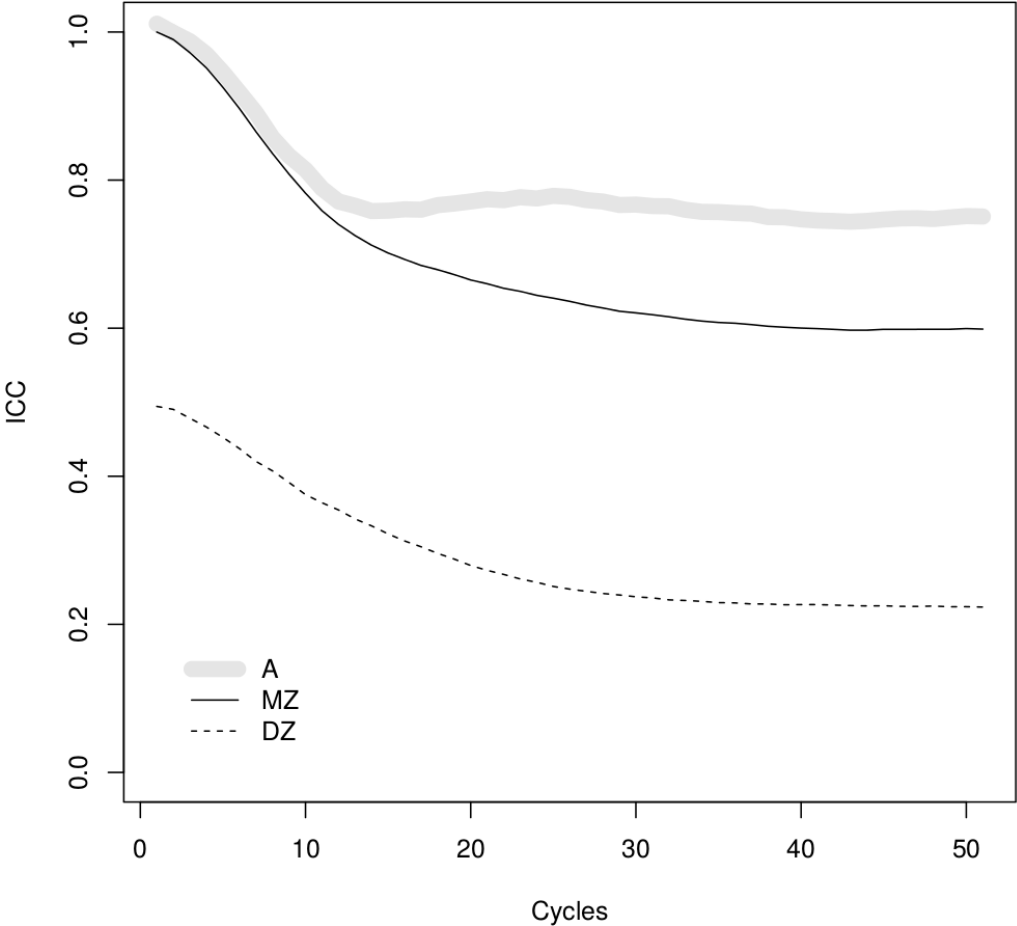
Heritability 10%, stable unique factors 10%, PET 80%



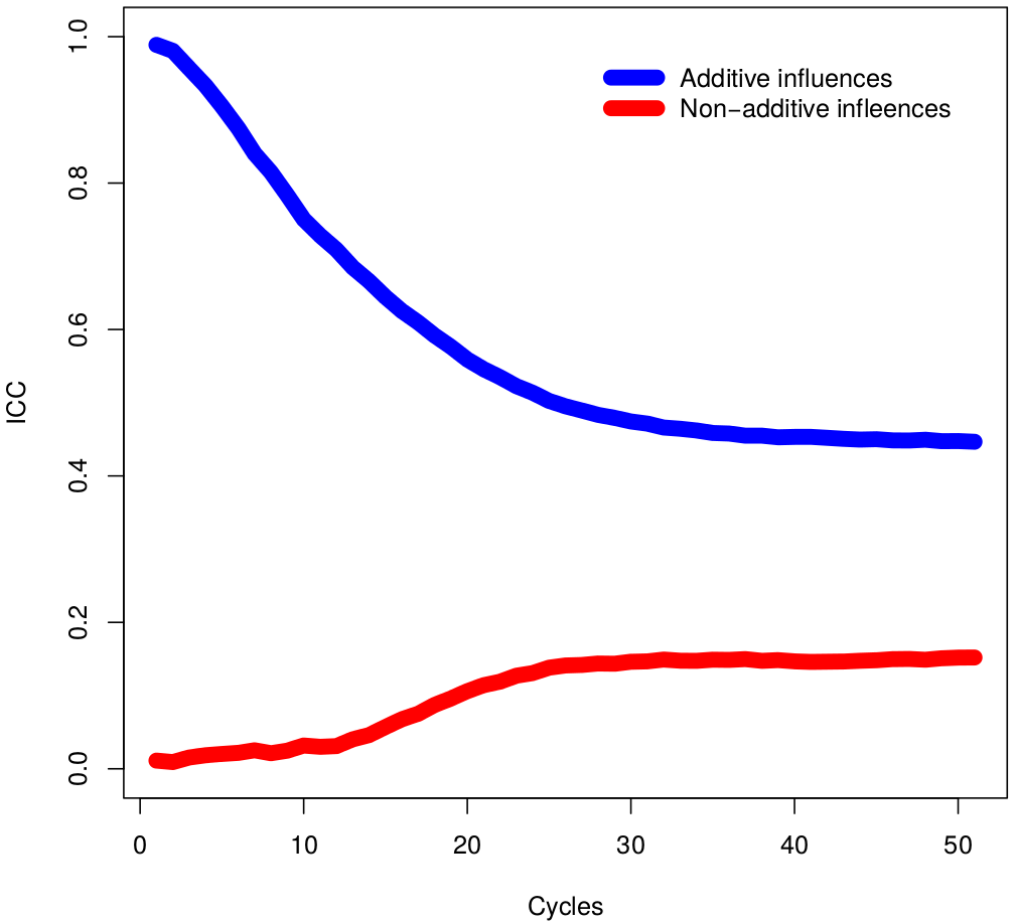
PET based on 25 most expressed traits

PET based on all traits

Heritability 10%, unique 10%, random 40%, PET 40% (50 traits)

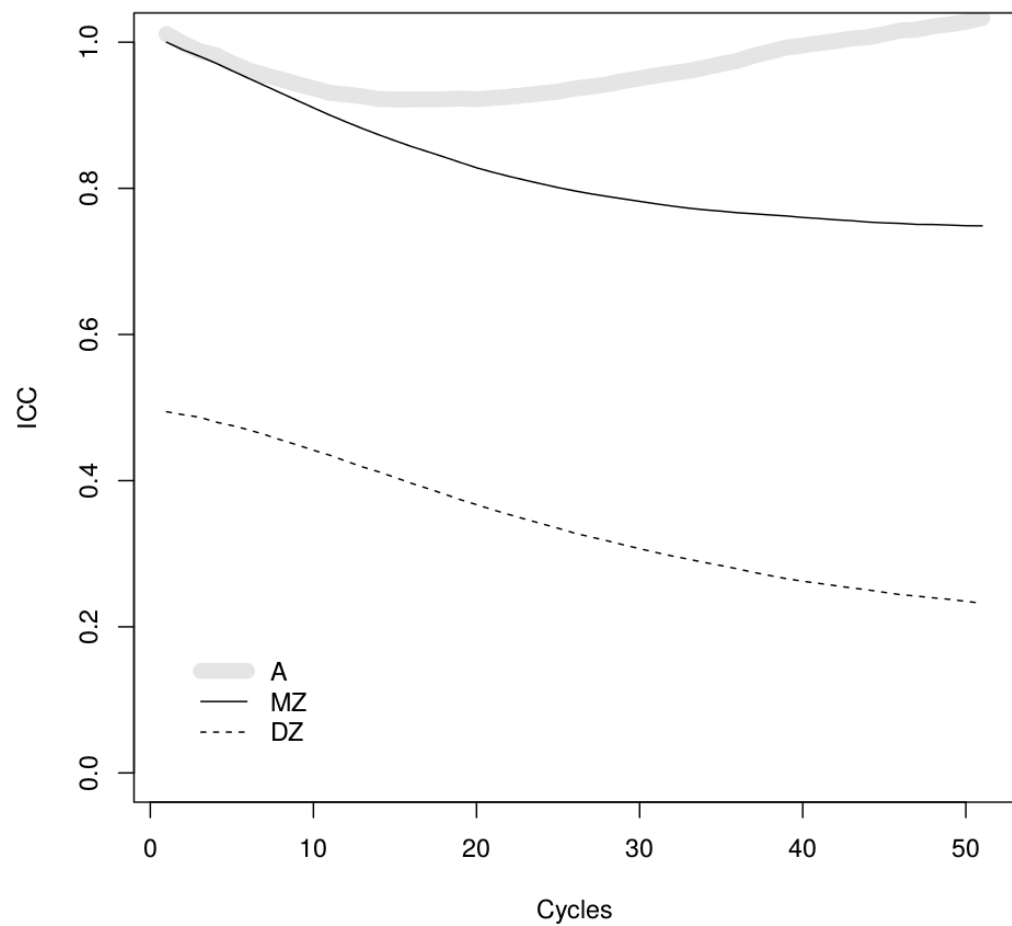


Heritability 10%, unique 10%, random 40%, PET 40% (50 traits)

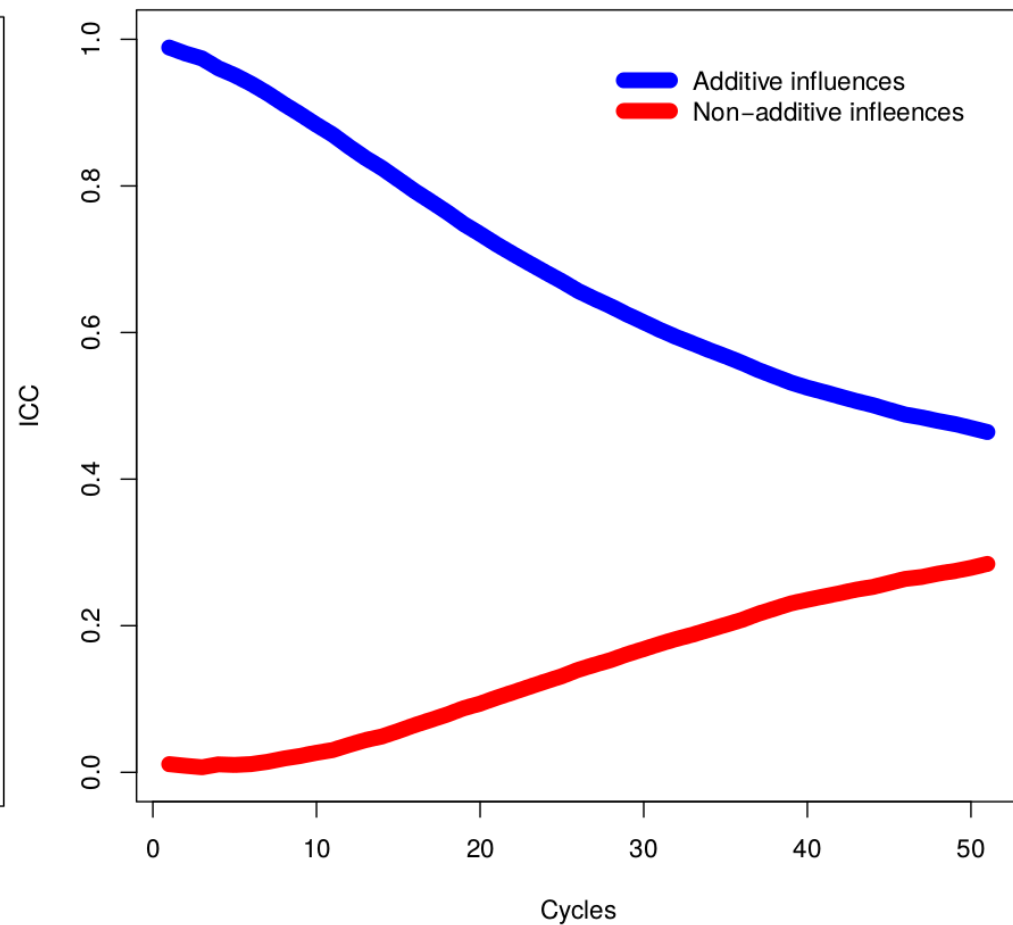


PET based on one trait
(the strongest absolute value)

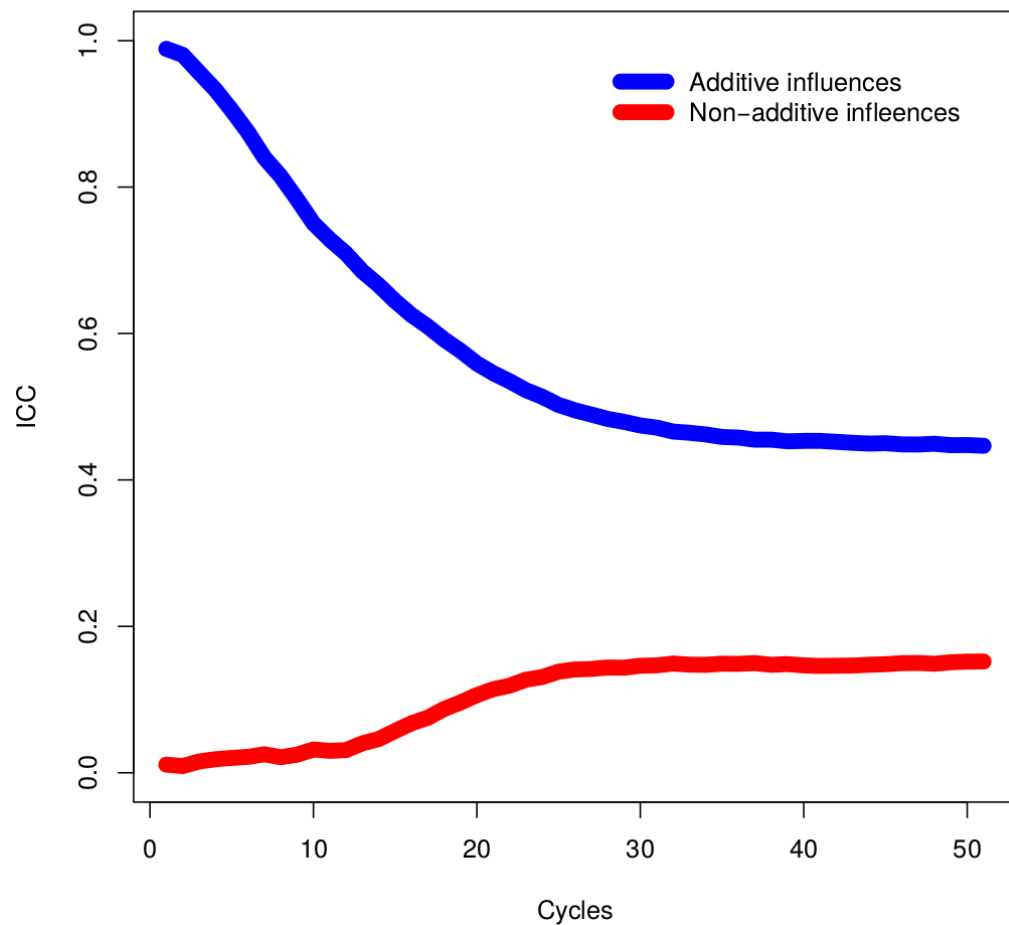
Heritability 10%, unique 10%, random 40%, PET 40% (one trait)



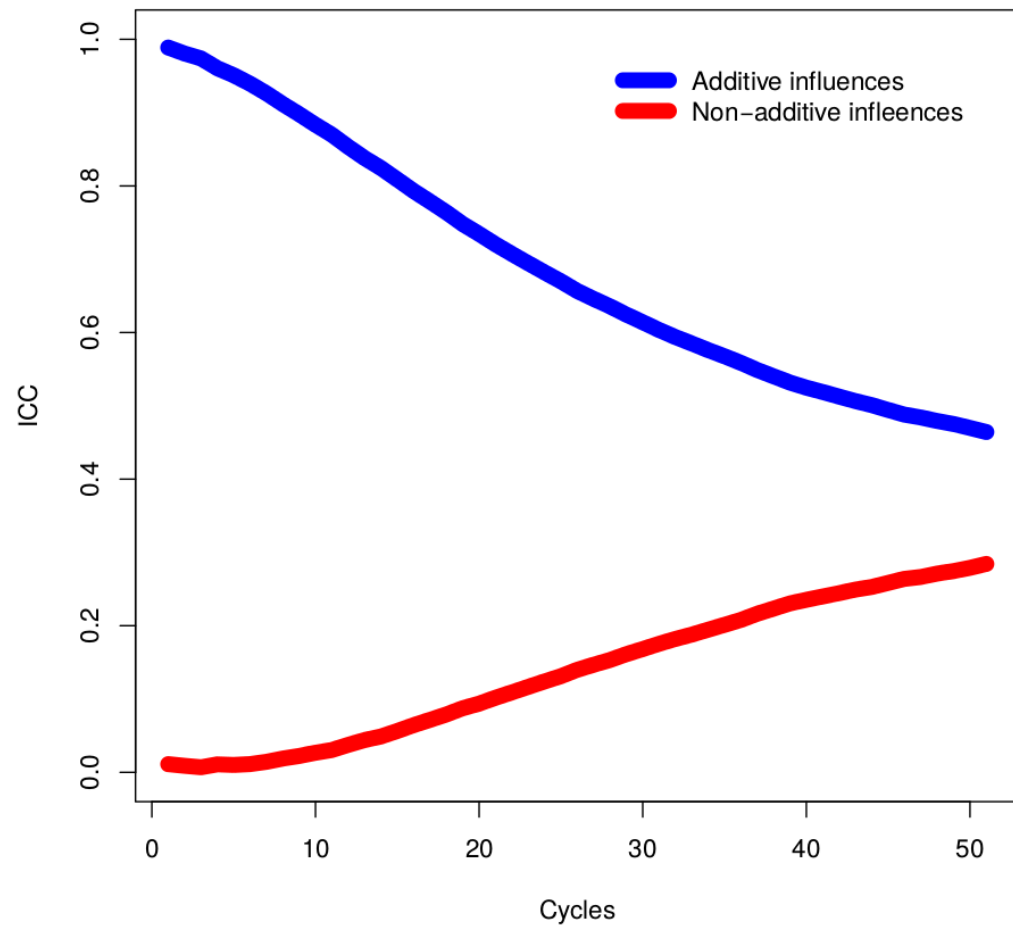
Heritability 10%, unique 10%, random 40%, PET 40% (one trait)



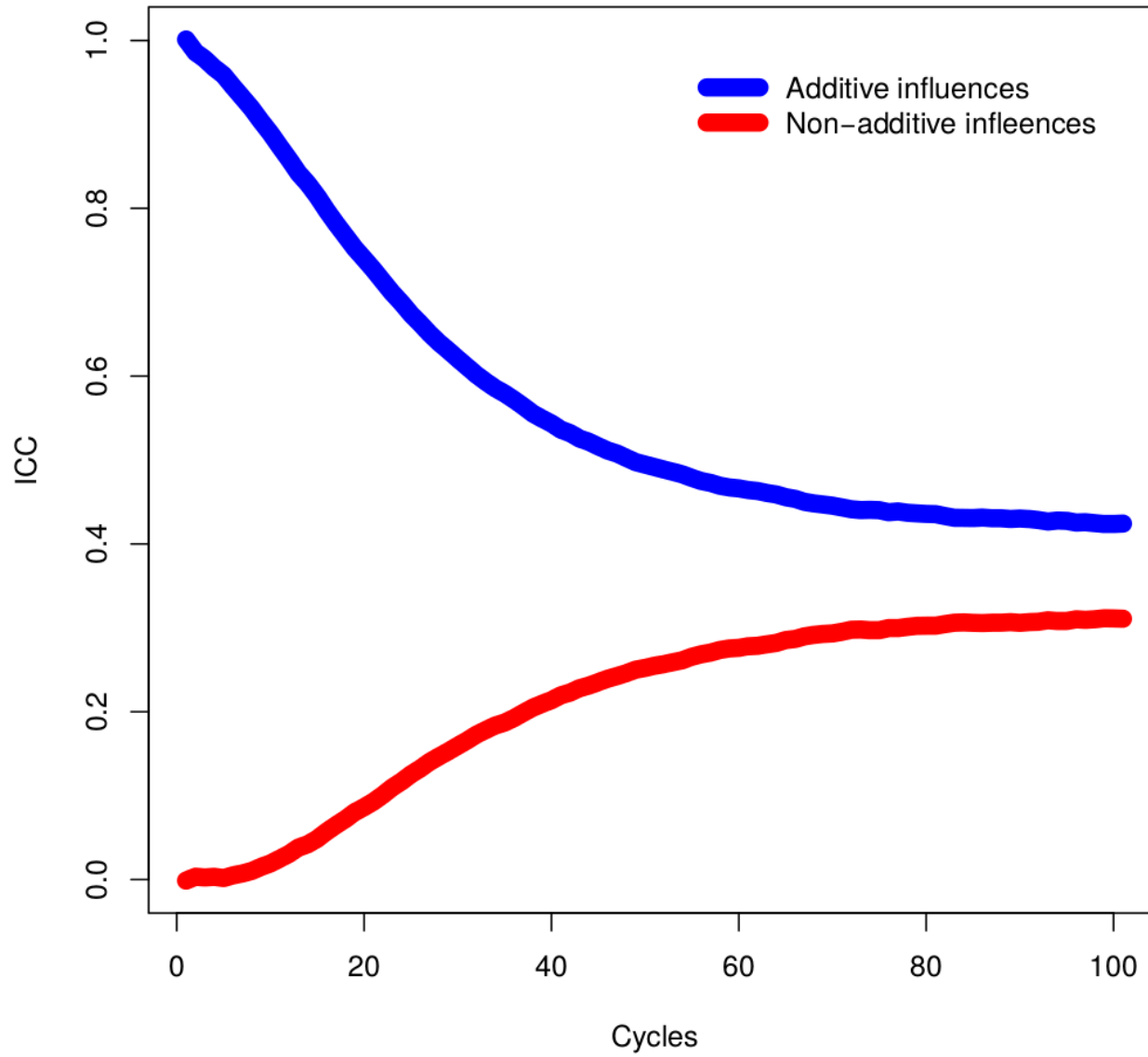
Heritability 10%, unique 10%, random 40%, PET 40% (50 traits)



Heritability 10%, unique 10%, random 40%, PET 40% (one trait)



Heritability 10%, unique 10%, random 40%, PET 40% (one trait)



PET can inflate heritability

- No news there
- But genetically similar people may become exponentially more similar
 - Especially when PET are idiosyncratic
 - 'Non-additive' genetic influence
 - No interactions between genetic variants involved

Computational models

- **Do not constitute evidence**
- But can be useful thinking tools
 - Play through ideas
 - Proof-of-principle testing
 - Can lead to testable hypotheses
- Implications for variance and 'factors'

Thanks to Mike Allerhand

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